

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 14, 2003, 04:41:21 ; Search time 0.674157 seconds

(Without alignments)
553.709 Million cell updates/sec

Title: US-09-698-781-17

Perfect score: 44
Sequence: 1 TLPVLLFL 9

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt.40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	44	100.0	245	1	CRS3_HUMAN
2	35	79.5	587	1	NDC2_RAT
3	34	77.3	247	1	DB83_HUMAN
4	34	77.3	247	1	DB83_RAT
5	34	77.3	301	1	REIS_TODPA
6	34	77.3	741	1	NMSC_FLARA
7	33	75.0	245	1	CRS3_HORSE
8	33	75.0	261	1	GILT_HUMAN
9	33	75.0	365	1	RECF_CHLNR
10	33	75.0	121	1	YDGF_ECOLI
11	32	72.7	405	1	CYB_RHORB
12	32	72.7	409	1	PEXC_PICPA
13	32	72.7	519	1	PEBT_CHICK
14	32	72.7	571	1	CVCA_PEA
15	32	72.7	100	1	VJPO_YEAST
16	31	70.5	154	1	YB6A_MERYA
17	31	70.5	170	1	Y019_BORBU
18	31	70.5	197	1	I17C_HUMAN
19	31	70.5	221	1	API1_SOLTU
20	31	70.5	221	1	API7_SOLTU
21	31	70.5	247	1	NU6M_WHEAT
22	31	70.5	324	1	NU1M_PISCO
23	31	70.5	428	1	KINB_BACSU
24	31	70.5	433	1	PSN1_XENLA
25	31	70.5	456	1	PTSB_KLEPN
26	31	70.5	456	1	PTSB_SALTU
27	31	70.5	467	1	PSN1_HUMAN
28	31	70.5	467	1	PSN1_MOUSE
29	31	70.5	467	1	PSN1_MOUSE
30	31	70.5	467	1	PSN1_MOUSE
31	31	70.5	468	1	PSN1_BOVIN
32	31	70.5	478	1	PSN1_BOVIN
33	31	70.5	499	1	MEP2_YEAST

34	31	70.5	517	1	HSF2_MOUSE	P38533 mus musculus
35	31	70.5	536	1	HSF2_HUMAN	Q03933 homo sapien
36	31	70.5	543	1	P69_MYCG	P47533 mycoplasma
37	31	70.5	564	1	HSF2_CHICK	P38530 gallus galli
38	31	70.5	679	1	PAN3_YEAST	P36102 saccharomyc
39	31	70.5	784	1	TIR2_CRIGR	Q971f8 cricetus
40	31	70.5	784	1	TUR2_MOUSE	Q94un7 mus musculus
41	31	70.5	1204	1	DNBI_VZVD	P09246 varicella-z
42	31	70.5	1816	1	LM44_HUMAN	Q16363 homo sapien
43	30	68.2	145	1	YVR9_YEAST	P53880 saccharomyc
44	30	68.2	153	1	ML1_CANFA	Q28296 canis famil
45	30	68.2	181	1	DSBE_PASMU	Q9cpm6 pasteurella

ALIGNMENTS

RESULT 1
ID CRS3_HUMAN STANDARD: PRT: 245 AA.
AC P54108; Q15512;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cysteine-rich secretory protein-3 precursor (CRISP-3) (SGP28 protein).
GN CRISP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE-96270732; PubMed-8665901;
RA Kretzschmar J., Haendler B., Eberspacher U., Roostermann D.,
Donner P., Schlenning W.-D.;
RT "The human cysteine-rich secretory protein (CRISP) family. Primary
structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3.";
RL Eur. J. Biochem. 236:827-836(1996).
[2]
RP MEDLINE-96186934; PubMed-8601434;
RA Kjeldsen L., Cowland J.B., Johnson A.H., Borregaard N.;
RT "SGP28, a novel matrix glycoprotein in specific granules of human
neutrophils with similarity to a human testis-specific gene product
and a rodent sperm-coating glycoprotein.";
RL FEBS Lett. 380:246-250(1996).
CC -I- SUBCELLULAR LOCATION: SECRETED; IN NEUTROPHILS, LOCALIZED IN
SPECIFIC GRANULES.
CC -I- TISSUE SPECIFICITY: SALIVARY GLAND, PANCREAS AND PROSTATE >
EPIDIDYMIS, OVARY, THYMUS AND COLON.
CC -I- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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CC EMBL: X95240; CAA64527.1; -;
CC EMBL: X94373; CAA63984.1; -;
CC HSSP: P04284; ICRB.
DR InterPro: IPR001283; Allrgn_V5/TPx1.
DR Pfam: PF00188; SCP. 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/TPx1. 1.
DR SMART: SM00198; SCP. 1.
DR PROSITE: PS01009; SCP_AGS_PRL_SCP_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SCP_2; 1.
DR Glycoprotein: Signal; Multigene family; Polymorphism.
FT SIGNAL 1 20 POTENTIAL.

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FT CHAIN 21 245 CYSTEINE-RICH SECRETORY PROTEIN-3.
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 106 106 S->P (IN DBSNP:495335).
FT VARIANT 134 134 /FTID-VAR.011718.
FT VARIANT 134 134 A->S (IN DBSNP:1864312).
FT SEQUENCE 245 AA; 27630 MW; BADD79CB/AE9E5F9 CRC64;

Query Match 100.0%; Score 44; DB 1; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLFPVLFL 9
Db 2 TLFPVLFL 10

RESULT 2
NDC2_RAT STANDARD: PRT: 587 AA.
AC P70545;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Intracellular sodium/dicarboxylate cotransporter (Na(+)/dicarboxylate
cotransporter).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RA MEDLINE=97107437; PubMed=8950177;
RA Klatra I.A., Kovacs S.V.B., Forstner J.F.;
RT Cloning of the cDNA for a rat intestinal Na+/dicarboxylate
cotransporter reveals partial sequence homology with a rat intestinal
mucin."
RL Blochys. Acta 1309:58-62(1996).
CC -1- FUNCTION: COTRANSPORT OF SODIUM AND DICARBOXYLATES SUCH AS
SUCCINATE AND CITRATE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE NADC/P/PHO87 FAMILY OF TRANSPORTERS.
CC NADC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U51153; AAB97095.1;
DR InterPro: IPR001898; Na_sulph_symp.
DR Pfam: PF00939; Na_sulph_symp; 1.
DR PROSITE: PS01271; NA_SULFATE; 1.
KW Transport; Transmembrane; Sodium transport; Symport.
FT TRANSMEM 13 33 POTENTIAL.
FT TRANSMEM 53 73 POTENTIAL.
FT TRANSMEM 120 140 POTENTIAL.
FT TRANSMEM 326 346 POTENTIAL.
FT TRANSMEM 367 387 POTENTIAL.
FT TRANSMEM 407 427 POTENTIAL.
FT TRANSMEM 445 465 POTENTIAL.
FT TRANSMEM 477 497 POTENTIAL.
FT TRANSMEM 506 526 POTENTIAL.
FT TRANSMEM 535 555 POTENTIAL.
SO SEQUENCE 587 AA; 63531 MW; F9B74F921BDC8712 CRC64;

Query Match 79.5%; Score 35; DB 1; Length 587;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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OY 2 LFPVLFL 9
Db 61 LFPVLFL 68

RESULT 3
DB83_HUMAN STANDARD: PRT: 247 AA.
ID DB83_HUMAN
AC P57088;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DB83 protein.
DE DB83.
GN DB83.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Nagatsuma M., Hosokawa T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,
RA Nimomiya K., Iwakatsuki T.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE UPF0121 FAMILY.
CC -----
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CC -----
DR EMBL: AK001387; BAA91665.1;
DR InterPro: IPR005344; UPF0121.
DR Pfam: PF03661; UPF0121; 1.
KW Transmembrane.
FT TRANSMEM 32 52 POTENTIAL.
FT TRANSMEM 101 121 POTENTIAL.
FT TRANSMEM 156 176 POTENTIAL.
SO SEQUENCE 247 AA; 27951 MW; 9C481A13ECCACB16 CRC64;

Query Match 77.3%; Score 34; DB 1; Length 247;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLFPVLFL 8
Db 111 SIFPVLFL 118

RESULT 4
DB83_RAT STANDARD: PRT: 247 AA.
ID DB83_RAT
AC Q92142;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DB83 protein.
DE DB83.
GN DB83.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE-99087491; PubMed-9672456;
RA Nakadai T., Kishimoto T., Kokura K., Ohkawa N., Makino Y.,
RA Muramatsu M., Tamura T.;
RT "Cloning of a novel rat gene, DB83, that encodes a putative membrane
RT protein."
RL DNA Res. 5:315-317(1998).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE LIVER AND
CC SIGNIFICANTLY IN BRAIN, LUNGS AND KIDNEYS.
CC -1- SIMILARITY: BELONGS TO THE UPR0121 FAMILY.
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DR EMBL; AB006135; BAA75068.1; -
DR InterPro: IPR005344; UPR0121.
DR Pfam; PF03661; UPR0121; 1.
KW Transmembrane.
FT TRANSMEM 32 52 POTENTIAL.
FT TRANSMEM 101 121 POTENTIAL.
FT TRANSMEM 156 176 POTENTIAL.
SQ SEQUENCE 247 AA; 27983 MW; 0D07BE5911CAD6AE CRC64;

Query Match 77.3%; Score 34; DB 1; Length 247;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LFPVLFL 8
Db 111 SLFVLFL 118

RESULT 5
REIS_TODPA STANDARD; PRT; 301 AA.
AC P23820;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Retinochrome (Retinal photoisomerase).
OS Todarodes pacificus (Japanese flying squid).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidae; Teuthoidea;
OC Oegopsida; Ommastrephidae; Todarodes.
OX NCBI_TaxID=6637;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-Retina;
RA MEDLINE-91032043; PubMed-2226795;
RA Hara-Nishimura I., Matsumoto T., Mori H., Nishimura M., Hara R.,
RA Hara T.;
RT "Cloning and nucleotide sequence of cDNA for retinochrome, retinal
RT photoisomerase from the squid retina."
RL FEBS Lett. 271:106-110(1990).
[2]
RN SEQUENCE OF 1-15 AND 114-128.
RP TISSUE-Retina;
RC TISSUE-Retina;
RA Uematsu J., Hara-Nishimura I., Wada K., Matsubara H., Hara T.;
RT "Amino-terminal sequence of squid retinochrome."
RL Photobiochem. Photobiophys. 13:197-201(1986).
[3]
RN SEQUENCE OF 274-281, AND RETINAL BINDING SITE.
RP TISSUE-Retina;
RA MEDLINE-94063090; PubMed-8243675;
RA Hara-Nishimura I., Kondo M., Nishimura M., Hara R., Hara T.;
RT "Amino acid sequence surrounding the retinal-binding site in
RT retinochrome of the squid, Todarodes pacificus."
RL FEBS Lett. 335:94-98(1993).
-1- FUNCTION: RETINOCROME IS CAPABLE OF ACTING AS AN EFFECTIVE

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CC CATALYST IN THE LIGHT TO CONVERT VARIOUS ISOMERS OF RETINAL
CC INTO 11-CIS, THE FORM THAT IS REQUIRED BY OPSIN TO RESYNTHESIZE
CC RHODOPSIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MYELOID MEMBRANE.
CC -1- TISSUE SPECIFICITY: MAINLY STORED IN MYELOID BODIES OF THE INNER
CC SEGMENTS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
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DR EMBL; X57143; CAA40422.1; -
DR PIR; S12864; S12864.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR001760; Opsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL1; FALSE_NEG.
DR PROSITE; PS50262; G-PROTEIN_RECEP_FL2; 1.
KW PROSITE; PS00238; OPSIN; 1.
KW Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision;
KW G-protein coupled receptor.
FT DOMAIN 1 17 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 18 43 1 (POTENTIAL).
FT DOMAIN 44 54 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 55 76 2 (POTENTIAL).
FT DOMAIN 77 94 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 95 120 3 (POTENTIAL).
FT DOMAIN 121 132 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 133 153 4 (POTENTIAL).
FT DOMAIN 154 180 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 181 208 5 (POTENTIAL).
FT DOMAIN 209 230 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 231 255 6 (POTENTIAL).
FT DOMAIN 256 264 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 265 289 7 (POTENTIAL).
FT DOMAIN 290 301 CYTOPLASMIC (POTENTIAL).
FT BINDING 275 275 RETINAL CHROMOPHORE.
FT CARBOHYD 170 170 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 301 AA; 33490 MW; CBB37317486B27FC CRC64;

Query Match 77.3%; Score 34; DB 1; Length 301;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 2 LFPVLFL 9
Db 280 LFPVLFL 287

RESULT 6
NU5C_FLARA STANDARD; PRT; 741 AA.
AC Q32238;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE NADH-plastoquinone oxidoreductase chain 5, chloroplast (EC 1.6.5.3).
OS NDH.
GN Flaveria ramosissima.
OC Flaveria.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eunsterids II; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Flaveria.
OX NCBI_TaxID=41578;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE-96036088; PubMed-7479788;
RA Kim K.J., Jansen R.K.;
RT "ndhf sequence evolution and the major clades in the sunflower
family.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:10379-10383(1995).
CC -1- CATALYTIC ACTIVITY: NADH + plastoquinone - NAD(+) + plastoquinol.
CC -----
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CC -----
CC EMBL; L39465; AAC37748.1;
CC InterPro: IPR003916; NADHoxrads.
CC InterPro: IPR001750; Oxidored_q1.
CC InterPro: IPR002128; Oxidored_q1_C.
CC InterPro: IPR001516; Oxidored_q1_N.
CC Pfam: PF00361; Oxidored_q1; 1.
CC Pfam: PF00662; Oxidored_q1_N; 1.
CC Pfam: PF01010; Oxidored_q1_C; 1.
CC PRINTS: PR01434; NADHoxrads.
CC OXIDOREDUCTASE; NAD; Plastoquinone; Chloroplast.
CC SEQUENCE 741 AA; 83948 MW; E0BD194ABEF0B9FB CRC64;
SO
Query Match 77.3%; Score 34; DB 1; Length 741;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Oy 2 LFPVLLFL 9
Db 549 LFPVLLFL 556

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RX EMBL; AJ001400; CA004729.1;
DR HSSP; P04284; ICEE.
DR InterPro: IPR001283; Allrgn_V5/TPx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPx1IKE.
DR PRODOM; PD000542; Allrgn_V5/TPx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AGS_PRL_SCT_1; 1.
DR PROSITE; PS01010; SCP_AGS_PRL_SCT_2; 1.
FW Signal: Multigene family.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 245 CYSTEINE-RICH SECRETORY PROTEIN-3.
SO SEQUENCE 245 AA; 27308 MW; 893A4EB87F402BA22 CRC64;
Query Match 75.0%; Score 33; DB 1; Length 245;
Best Local Similarity 87.5%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 2 LFPVLLFL 9
Db 3 LFPVLLFL 10

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RESULT 8

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ID GILT_HUMAN STANDARD; PRT; 261 AA.
AC P13284; Q9UL08;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gamma-interferon inducible lysosomal thiol reductase precursor
DE (Gamma-interferon-inducible protein IP-30).
GN IFI30 OR GILT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-88298888; PubMed-3136170;
RA Luster A.D., Welshshank R.L., Felman R., Ravetch J.V.;
RT "Molecular and biochemical characterization of a novel gamma-
RT interferon-inducible protein.";
RL J. Biol. Chem. 263:12036-12043(1988).
RN [2]
RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
RX MEDLINE-20105543; PubMed-10639150;
RA Arunachalam B., Phan U.T., Geuze H.J., Cresswell P.;
RT "Enzymatic reduction of disulfide bonds in lysosomes: characterization
RT of a gamma-interferon-inducible lysosomal thiol reductase (GILT).";
RL Proc. Natl. Acad. Sci. U.S.A. 97:745-750(2000).
CC -1- FUNCTION: CLEAVES DISULFIDE BONDS IN PROTEINS BY REDUCTION. MAY
CC FACILITATE THE COMPLETE UNFOLDING OF PROTEINS DESTINED FOR
CC LYSOSOMAL DEGRADATION. MAY BE INVOLVED IN MHC CLASS II-RESTRICTED
CC ANTIGEN PROCESSING.
CC -1- SUBCELLULAR LOCATION: Lysosomal.
CC -1- INDUCTION: EXPRESSED CONSTITUTIVELY IN ANTIGEN-PRESENTING CELLS
CC AND INDUCED BY IFN-GAMMA IN OTHER CELL TYPES.
CC -1- PTM: N-GLYCOSYLATED. SUGAR CHAINS CONTAIN MANNOSE-6-PHOSPHATE.
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CC -----
CC EMBL; J03909; AA36105.1;
CC EMBL; AF097362; AA04618.1;
CC PIR; A43708; A43708.
CC Genew; HGNC:5398; IFI30.
CC MIM; 604664;

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DR InterPro: IPR001238; Refc.
DR InterPro: IPR003395; SMC_N.
DR Pfam: PF02463; SMC_N; 1.
DR TIGRfams: TIGR00611; Refc; 1.
DR PROSITE: PS00617; Refc_1; 1.
DR PROSITE: PS00618; Refc_2; 1.
KW DNA damage; DNA replication; DNA-binding; SOS response; DNA repair;
KW ATP-binding; Complete proteome.
FT NP_BIND 30
SQ SEQUENCE 365 AA: 41321 MW: F097CE97810C8958 CRC64:

Query Match
Best Local Similarity 75.0%; Score 33; DB 1; Length 365;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LEPUVF 8
DB 110 LEPUVF 116

RESULT 10
REFC_CHLTR STANDARD: PRT: 365 AA.
AC 084077;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA replication and repair protein refc.
DE Refc OR CT074.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxId=813;
RX MEDLINE=99008089; PubMed=9784136;
RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Davis R.W., Olinger L., Tatusov R.L., Zhao Q., Koehn E.V.,
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
CC -1- FUNCTION: THE RECF PROTEIN IS INVOLVED IN DNA METABOLISM; IT IS
CC REQUIRED FOR DNA REPLICATION AND NORMAL SOS INDUCIBILITY. RECF
CC BINDS PREFERENTIALLY TO SINGLE-STRANDED, LINEAR DNA. IT ALSO SEEMS
CC TO BIND ATP (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE RECF FAMILY.
-----
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-----
CC EMBL: AE001282; AAC67665.1;
CC InterPro: IPR001238; Refc.
CC InterPro: IPR003395; SMC_N.
CC Pfam: PF02463; SMC_N; 1.
CC TIGRfams: TIGR00611; Refc; 1.
CC PROSITE: PS00617; Refc_1; 1.
CC PROSITE: PS00618; Refc_2; 1.
KW DNA damage; DNA replication; DNA-binding; SOS response; DNA repair;
KW ATP-binding; Complete proteome.
FT NP_BIND 30
SQ SEQUENCE 365 AA: 41246 MW: CC058A9475638A0B CRC64:

Query Match
Best Local Similarity 75.0%; Score 33; DB 1; Length 365;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY      2 LFPVLF 8
Db      110 LFPVLF 116

RESULT 11
YDGF_ECOLI
ID YDGF_ECOLI STANDARD: PRT: 121 AA.
AC P77412;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydGF.
GN YDGF OR B1600 OR Z2594 OR ECS2306.
OS Escherichia coli, and
OC Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562, 83334;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE-9742617; PubMed-9278503;
RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Valdes J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE-9725137; PubMed-9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kasai H., Kashiwano K., Kimura S., Kitakawa M.,
RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
RA Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y.,
RA Oshima T., Saito N., Sampei G., Seki Y., Sivasubram S.,
RA Tagami H., Takeda J., Takekoshi K., Takeuchi Y., Wada C.,
RA Yamamoto Y., Horiiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN
RP SEQUENCE FROM N.A.
RC STRAIN-O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE-21074935; PubMed-11256551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boulton A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lam A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Weich R.A., Blatter F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN
RP SEQUENCE FROM N.A.
RC STRAIN-O157:H7 / RIMD 0509952;
RX MEDLINE-21156231; PubMed-11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsuo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kunara S., Shiba T., Hattoni M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN
RP SUBCELLULAR LOCATION: Integral membrane protein (Potential).
RN
RP SIMILARITY: BELONGS TO THE SMALL MOULTINROG RESISTANCE (SMR)
PROTEIN FAMILY.
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CC
CC -----
DR EMBL: AE000255; AAC74672.1; -
DR EMBL: D90803; BAA15339.1; -
DR EMBL: D90802; BAA15334.1; -
DR EMBL: AE005383; AAG56587.1; -
DR EMBL: AP002558; BAB35729.1; -
DR EcoGene: EG13927; ydGF.
DR InterPro: IPR000390; DUF7.
DR Pfam: PF00893; DUF7; 1.
KW Hypothetical protein; Transmembrane; Transport; Complete proteome.
FT TRANSMEM 2 22
FT TRANSMEM 32 52 POTENTIAL.
FT TRANSMEM 55 75 POTENTIAL.
FT TRANSMEM 82 102 POTENTIAL.
SO SEQUENCE 121 AA; 13115 MW; B24330AF5BB181B5 CRC64;

Query Match 72.7%; Score 32; DB 1; Length 121;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 TLFPVLF 8
Db      73 TLFPVLF 80

RESULT 12
CYB_RHORO
ID CYB_RHORO STANDARD: PRT: 405 AA.
AC P23134;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome B.
GN Cytochrome B.
OS Rhodospirillum rubrum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
OC Rhodospirillum.
OX NCBI_Taxid=1085;
RN
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-27.
RC STRAIN-FRI;
RX MEDLINE-91094774; PubMed-2176269;
RA Majewski C., Trebst A.;
RT "The pet genes of Rhodospirillum rubrum: cloning and sequencing of
the genes for the cytochrome bcl-complex.";
RL Mol. Gen. Genet. 224:373-382(1990).
RN
RP FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS.
CC COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN.
CC - SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
CC - SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
CC
CC -----
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CC
CC -----
DR EMBL: X55387; CAA39059.1; -
DR PIR: S12257; CBOFR.
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00033; cytochrome_b_c1.
DR Pfam: PF00033; cytochrome_b_n_1.

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DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
 DR PROSITE: PS00193; CYTOCHROME_B_OO; 1.
 KM Electron transport; Respiratory chain; Heme; Transmembrane.
 FT METAL 94 94 IRON 1 (HEME B562 AXIAL LIGAND).
 FT METAL 108 108 IRON 2 (HEME B566 AXIAL LIGAND).
 FT METAL 195 195 IRON 2 (HEME B566 AXIAL LIGAND).
 FT METAL 209 209 IRON 1 (HEME B566 AXIAL LIGAND).
 SQ SEQUENCE 405 AA; 46369 MW; F19452EDA118BE6F CRC64;

Query Match 72.7%; Score 32; DB 1; Length 405;
 Best Local Similarity 85.7%; Pred. No. 63;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LFPVLLF 8
 DB 197 LFPVLLF 203

RESULT 13
 PEPC_PICPA STANDARD; PRT; 409 AA.
 AC 001961;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peroxisome assembly protein PAS10 (Peroxin-12).
 GN PEX12 OR PAS10.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 OX NCBI_TaxID=4922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96283626; PubMed=8670828;
 RA Kalish J.E., Keller G.-A., Morrell J.C., Mihalik S.J., Smith B.,
 RA Clegg J.M., Gould S.J.;
 RT "Characterization of a novel component of the peroxisomal protein
 RT import apparatus using fluorescent peroxisomal proteins."
 RL EMBL J.1533275-3285(1996).
 CC -1- FUNCTION: REQUIRED FOR PROTEIN IMPORT INTO PEROXISOMES.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Peroxisomal.
 CC -1- SIMILARITY: BELONGS TO THE PEROXIN 12 FAMILY.
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 CC -----
 CC EMBL: U58140; AAC49402.1; -
 DR InterPro: IPR001841; Znf_Lfing.
 DR SMART: SM00184; RING; 1.
 KM Transmembrane; Peroxisome.
 FT TRANSMEM 171 191
 FT TRANSMEM 267 287 POTENTIAL.
 SQ SEQUENCE 409 AA; 47591 MW; 1F2DB79A957C3B7F CRC64;

Query Match 72.7%; Score 32; DB 1; Length 409;
 Best Local Similarity 66.7%; Pred. No. 64;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 TLFPVLLF 9
 DB 273 TLFPASIFL 281

RESULT 14
 PPBT_CHICK STANDARD; PRT; 519 AA.
 ID PPBT_CHICK
 AC 092058;
 DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Alkaline phosphatase, tissue-nonspecific isozyme precursor
 DE (EC 3.1.3.1) (AP-TNAP) (Liver/Bone/Kidney isozyme).
 GN ALPL.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96107571; PubMed=8563025;
 RA Crawford K., Weisig H., Binette F., Millan J.L., Goetlinc P.F.;
 RT "Tissue-nonspecific alkaline phosphatase participates in the
 RT establishment and growth of feather germs in embryonic chick skin
 RT cultures."
 RL Dev. Dyn. 204:48-56(1995).
 CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
 CC alcohol + phosphate.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ALKALINE PHOSPHATASE FAMILY.
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 CC -----
 CC EMBL: U91908; AAA92562.1; -
 DR HSSP: P00634; 2ANR.
 DR InterPro: IPR001952; Alk-phosphatse.
 DR Pfam: PF00245; alk-phosphatase; 1.
 DR PRINTS: PR00113; ALKPHPTASE.
 DR ProDom: PD001668; Alk-phosphatse; 1.
 DR SMART: SM00098; alkPrc; 1.
 DR PROSITE: PS00123; ALKALINE_PHOSPHATASE; 1.
 KM Hydrolyase; zinc; Magnesium; Phosphorylation; Transmembrane;
 KM Multigene family; Glycoprotein; GPI-anchor; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 519
 FT MOD_RES 109 109
 FT ACT_SITE 109 109
 FT CARBOHYD 139 139
 FT CARBOHYD 229 229
 FT CARBOHYD 278 278
 FT CARBOHYD 302 302
 FT CARBOHYD 429 429
 SQ SEQUENCE 519 AA; 56760 MW; 7934C0EBC3B17889 CRC64;

Query Match 72.7%; Score 32; DB 1; Length 519;
 Best Local Similarity 77.8%; Pred. No. 80;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TLFPVLLF 9
 DB 507 TLFPVLLF 515

RESULT 15
 CVCA_PEA STANDARD; PRT; 571 AA.
 ID CVCA_PEA
 AC P13915;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Convallin precursor.
 GN CVCA.

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OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID:3888;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=cv. Feltham First;
RX MEDLINE:88326208; PubMed:3415641;
RA Bown D., Ellis T.H.N., Gatehouse J.A.;
RT "The sequence of a gene encoding convicillin from pea (Pisum sativum
RT L.) shows that convicillin differs from vicillin by an insertion near
RL Biochem. J. 251:717-726(1988).
CC -!- FUNCTION: SEED STORAGE PROTEIN.
CC -!- SUBCELLULAR LOCATION: CYTOLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
CC BODIES.
CC -!- SIMILARITY: BELONGS TO THE 7S SEED STORAGE PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL: X06398; CAA29695.1; -.
DR PIR: S00566; S00566.
DR HSSP: P02853; 2PHL.
DR InterPro: IPR001113; Seedstore_7s.
DR Pfam: PF00546; Seedstore_7s; 1.
DR Pfam: PF02808; Seedstore_7s_C; 1.
KW Seed storage protein; Multigene family; Signal.
FT SIGNAL 1 28
FT CHAIN 29 571 CONVICILIN.
SQ SEQUENCE 571 AA; 66989 MW; 749CFEBB2D16D57B CRC64;

Query Match 72.7%; Score 32; DB 1; Length 571;
Best Local Similarity 85.7%; Pred. NO. 88;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 FVLLFL 9
   11:1111
DB 9 FVLLFL 15

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Search completed: March 14, 2003, 05:40:56
 Job time : 1.67416 secs